A computer based method for identifying peptides useful as drug targets

Abstract

The present invention relates to a novel computer based method for performing genome-wise comparison of several organisms, the said computational method involves creation of peptide libraries from protein sequences of several organisms and subsequent comparison leading to identification of conserved invariant peptide motifs, and to this end several invariant peptide motifs have been identified by direct sequence comparison between various bacterial organisms and host genomes without any *a priori* assumptions, and the present method is useful for identification of potential drug targets and can serve as drug screen for broad-spectrum antibacterials as well as for specific diagnosis of infections, and in addition, for assignment of function to proteins of yet unknown functions with the help of such invariant peptide motif signatures.